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<110> Zhou, Pengbo
Howley, Peter M.

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<141> 1999-10-08

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<213> *Saccharomyces cerevisiae*

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<213> *Saccharomyces cerevisiae*

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Phe Arg Phe Asp Ser Ile Gln Arg Glu Thr Leu Leu Pro Thr Asn Asn
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Glu Leu Arg Ile Asp Asn Ser Pro Gln Ala Ile Ser Tyr Leu His Lys
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Leu Gln Arg Met Arg Leu Arg Ala Leu Glu Thr Glu Asn Met Glu Ile
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Glu Ser Ser Asp Leu Lys Glu Gly Leu Gln Asp Leu Ser Arg Tyr Ser
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Val Lys Ile Leu Tyr Tyr Arg Pro His Ile Asn Lys Lys Ser Gln Leu
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Asp Leu Phe Leu Arg Thr Met Lys Leu Thr Ser Glu Glu Thr Val Phe
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Asn Tyr Arg Leu Met Ile Lys Arg Leu Asn Phe Ser Phe Val Gly Asp
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Tyr Met His Asp Thr Glu Leu Asn Tyr Phe Val Gly Cys Lys Asn Leu
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Ser Ala Val Leu Arg Gly Cys Lys Phe Leu Gln Ser Val Asp Ile Thr
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<213> *Saccharomyces cerevisiae*

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ccattaatgg ttttgccgtc taattcaggc tacattagta gctttgtgtc agatgaacac 1920
aaaattatta gtggaatga tggttctgta aagttatggg atgttaggac tggaaagctg 1980
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<210> 10

<211> 703

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

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Met Ser Leu Ser Arg Cys Pro Thr Asp Asn Ser Ser Ser Arg Ile Asn
  1                      5                      10                      15

Ser Ser Val Pro Leu Ile Asn Ser Ser Ser Pro Ala Thr Pro Pro Glu
                20                      25                      30

Ser Phe Asp Pro Gln Val Phe Pro Ser Ser Leu Ile His Gly Asp Asn
  35                      40                      45

Leu Leu Pro Gln Asp Asp Gln Ile Ala Ser Asp Pro Arg Ser Glu Ser
  50                      55                      60

Asn Ser Cys Asn Gly Asn Thr Ser Ser Ser Leu Pro Cys Thr Asp Ser
  65                      70                      75                      80

Tyr Gln Tyr Pro Leu Lys His Ser Cys Thr Pro Ser Phe Leu Arg Lys
                85                      90                      95

Phe Asn Glu Ser Ile Glu Asn Val Ser Tyr Lys Cys Leu Asp His Ser
  100                      105                      110

Pro Pro Asp Ser Val Pro Gly Asp Phe Ser Ile Ser Leu Val Pro Gln
  115                      120                      125

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Arg Asn Phe Leu Tyr Ser His Ser Ser Leu Pro Pro Lys Ile Ile Ser
 130 135 140
 Ile Asp Arg Asn Asn Arg Ile Lys Leu Asp Asn Ser Ile Ser Ser Asn
 145 150 155 160
 Ser Asp Asn Phe Pro Pro Ser Pro Lys Val Asp Thr Ser Asn Thr Val
 165 170 175
 Ser Pro Gly Ser Lys Pro Ile Ser Glu Asp Leu Glu Asp Leu Asn Leu
 180 185 190
 Gln Ser Ile Val Gln Thr Phe Glu Asp Leu Pro Glu Gly Ile Gln Ser
 195 200 205
 Tyr Ala Phe Phe Gln Leu Leu Arg Ser Cys Asn Arg Gln Ser Met Arg
 210 215 220
 Leu Leu Leu Asn Glu Cys Glu Pro Leu Leu Lys Lys Asp Ile Leu Ser
 225 230 235 240
 Asn Leu Pro Phe Ser Ile Val Gln Ser Ile Leu Leu Asn Leu Asp Ile
 245 250 255
 His Ser Phe Leu Ser Cys Arg Leu Val Ser Pro Thr Trp Asn Arg Ile
 260 265 270
 Leu Asp Val His Thr Ser Tyr Trp Lys His Met Phe Ser Leu Phe Gly
 275 280 285
 Phe Gln Ile Asn Glu Asn Asp Trp Lys Tyr Ala Asn Pro Asn Leu Asn
 290 295 300
 Arg Pro Pro Phe Leu His Asn Asp Gln Ile Ser Asp Asp Tyr Phe Pro
 305 310 315 320
 Glu Ile Phe Lys Arg His Phe Leu Asn Arg Lys Arg Trp Leu Phe Pro
 325 330 335
 Ser Ile Pro Pro Ser His Leu Ser Phe Pro Ile His Val Pro Asn Phe
 340 345 350
 Met Ile Thr Ser Leu Leu Leu His Lys Asp Arg Ile Ile Thr Thr Ser
 355 360 365
 Gly Ser Gly Thr Ile Gln Ile His Asn Ala Ile Thr Gly Val Leu Glu
 370 375 380
 Ala Arg Leu Glu Gly His Lys Glu Gly Val Trp Ala Val Lys Ile His
 385 390 395 400
 Glu Asn Thr Leu Val Ser Gly Ser Ile Asp Lys Thr Val Arg Val Trp
 405 410 415
 Asn Ile Glu Lys Ala Lys Cys Thr His Ile Phe Arg Gly His Ile Ser
 420 425 430

Ile Ile Arg Cys Leu Glu Ile Leu Val Pro Ser Arg Leu Ile Arg His
 435 440 445
 Gly Val Glu Ile Val Glu Pro Asp Gln Pro Tyr Ile Val Ser Gly Ser
 450 455 460
 Arg Asp His Thr Leu Arg Val Trp Lys Leu Pro Lys Asn Thr Asp Pro
 465 470 475 480
 Pro Tyr Leu Pro Asp Asn Thr Asn Ser Ile Asp Arg Trp Glu Lys Asn
 485 490 495
 Pro Tyr Phe Val His Thr Leu Ile Gly His Thr Asp Ser Val Arg Thr
 500 505 510
 Ile Ser Gly Tyr Gly Asp Ile Leu Val Ser Gly Ser Tyr Asp Ser Ser
 515 520 525
 Ile Arg Ile Trp Arg Val Ser Thr Gly Glu Cys Leu Tyr His Leu Arg
 530 535 540
 Gly His Ser Leu Arg Ile Tyr Ser Val Leu Tyr Glu Pro Glu Arg Asn
 545 550 555 560
 Ile Cys Ile Ser Gly Ser Met Asp Lys Ser Ile Arg Val Trp Asp Leu
 565 570 575
 Ser Thr Gly Thr Cys Lys Tyr Val Leu Glu Gly His Asp Ala Phe Val
 580 585 590
 Thr Leu Leu Asn Val Phe Gln Asn Arg Leu Ile Ser Gly Ser Ala Asp
 595 600 605
 Ser Thr Ile Arg Ile Trp Asp Leu Asn Thr Gly Lys Pro Leu Met Val
 610 615 620
 Leu Pro Ser Asn Ser Gly Tyr Ile Ser Ser Phe Val Ser Asp Glu His
 625 630 635 640
 Lys Ile Ile Ser Gly Asn Asp Gly Ser Val Lys Leu Trp Asp Val Arg
 645 650 655
 Thr Gly Lys Leu Leu Arg Phe Leu Leu Thr Asp Leu Thr Lys Ile Trp
 660 665 670
 His Val Asp Phe Asp Ala Met Arg Cys Val Ala Ala Val Gln Arg Asp
 675 680 685
 Asp Gln Ala Tyr Leu Glu Val Ile Asn Phe Ser Gly Ser Arg Pro
 690 695 700

<210> 11
 <211> 2175
 <212> DNA
 <213> Murine sp.

<400> 11

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aggaagataa taccagagaa gaattcactt agacagactt acaacagctg tgccaggctt 240
tgcataaacc aagagacagt atgtctaaca agcactgcta tgaagactga aaattgtgtg 300
gccaaagcca aacttgccaa tggcacttcc agcatgattg tgcccaagca gcggaaactc 360
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gctgctgagc tcgtgtgcaa ggaatggtag cgctgacgt cggacggcat gctgtggaaa 660
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<210> 12

<211> 569

<212> PRT

<213> Murine sp.

<400> 12

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Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met
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Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
      20              25              30

Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
      35              40              45

Arg Leu Cys Ile Asn Gln Glu Thr Val Cys Leu Thr Ser Thr Ala Met
      50              55              60

```

Lys	Thr	Glu	Asn	Cys	Val	Ala	Lys	Ala	Lys	Leu	Ala	Asn	Gly	Thr	Ser	
65					70					75					80	
Ser	Met	Ile	Val	Pro	Lys	Gln	Arg	Lys	Leu	Ser	Ala	Ser	Tyr	Glu	Lys	
				85					90					95		
Glu	Lys	Glu	Leu	Cys	Val	Lys	Tyr	Phe	Glu	Gln	Trp	Ser	Glu	Ser	Asp	
			100					105					110			
Gln	Val	Glu	Phe	Val	Glu	His	Leu	Ile	Ser	Gln	Met	Cys	His	Tyr	Gln	
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His	Gly	His	Ile	Asn	Ser	Tyr	Leu	Lys	Pro	Met	Leu	Gln	Arg	Asp	Phe	
	130					135					140					
Ile	Thr	Ala	Leu	Pro	Ala	Arg	Gly	Leu	Asp	His	Ile	Ala	Glu	Asn	Ile	
145					150					155					160	
Leu	Ser	Tyr	Leu	Asp	Ala	Lys	Ser	Leu	Cys	Ala	Ala	Glu	Leu	Val	Cys	
				165					170					175		
Lys	Glu	Trp	Tyr	Arg	Val	Thr	Ser	Asp	Gly	Met	Leu	Trp	Lys	Lys	Leu	
			180						185					190		
Ile	Glu	Arg	Met	Val	Arg	Thr	Asp	Ser	Leu	Trp	Arg	Gly	Leu	Ala	Glu	
		195					200					205				
Arg	Arg	Gly	Trp	Gly	Gln	Tyr	Leu	Phe	Lys	Asn	Lys	Pro	Pro	Asp	Glu	
		210				215					220					
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225					230					235					240	
Gln	Asp	Ile	Glu	Thr	Ile	Glu	Ser	Asn	Trp	Arg	Cys	Gly	Arg	His	Ser	
				245					250					255		
Leu	Gln	Arg	Ile	His	Cys	Arg	Ser	Glu	Thr	Ser	Lys	Gly	Val	Tyr	Cys	
			260						265				270			
Leu	Gln	Tyr	Asp	Asp	Gln	Lys	Ile	Val	Ser	Gly	Leu	Arg	Asp	Asn	Thr	
		275					280					285				
Ile	Lys	Ile	Trp	Asp	Lys	Ser	Thr	Leu	Glu	Cys	Lys	Arg	Ile	Leu	Thr	
	290					295					300					
Gly	His	Thr	Gly	Ser	Val	Leu	Cys	Leu	Gln	Tyr	Asp	Glu	Arg	Val	Ile	
305					310					315					320	
Ile	Thr	Gly	Ser	Ser	Asp	Ser	Thr	Val	Arg	Val	Trp	Asp	Val	Asn	Ala	
				325					330					335		
Gly	Glu	Met	Leu	Asn	Thr	Leu	Ile	His	His	Cys	Glu	Ala	Val	Leu	His	
			340					345					350			
Leu	Arg	Phe	Asn	Asn	Gly	Met	Met	Val	Thr	Cys	Ser	Lys	Asp	Arg	Ser	
		355					360					365				

Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg
 370 375 380
 Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp
 385 390 395 400
 Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn
 405 410 415
 Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly
 420 425 430
 Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser
 435 440 445
 Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg
 450 455 460
 Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn
 465 470 475 480
 Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp
 485 490 495
 Leu Met Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu
 500 505 510
 Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp
 515 520 525
 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp
 530 535 540
 Asp Phe Leu Asn Asp Pro Ala Ala His Ala Glu Pro Pro Arg Ser Pro
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 Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
 565

<210> 13

<211> 9

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: peptide motif

<400> 13

Pro Pro Lys Lys Lys Arg Lys Val Ala

1

5

<210> 14

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: formula
sequence

<220>

<221> MOD_RES

<222> (3)...(6)

<223> any amino acid

<220>

<221> MOD_RES

<222> (7)

<223> hydrophobic amino acid

<220>

<221> MOD_RES

<222> (8)...(9)

<223> any amino acid

<220>

<221> MOD_RES

<222> (10)

<223> hydrophobic amino acid

<220>

<221> MOD_RES

<222> (11)

<223> any amino acid

<220>

<221> MOD_RES

<222> (12)

<223> aromatic amino acid

<220>

<221> MOD_RES

<222> (13)

<223> any amino acid

<220>

<221> MOD_RES

<222> (14)...(16)

<223> amino acid which stabilizes a tight polypeptide
backbone turn such as gly, pro, asp or asn

<220>

<221> MOD_RES

<222> (17)

<223> polar amino acid

<220>

<221> MOD_RES

<222> (18)

<223> any amino acid

<220>
 <221> MOD_RES
 <222> (19)...(20)
 <223> hydrophobic amino acid

<220>
 <221> MOD_RES
 <222> (21)...(24)
 <223> any amino acid

<220>
 <221> MOD_RES
 <222> (26)...(29)
 <223> any amino acid

<220>
 <221> MOD_RES
 <222> (30)
 <223> hydrophobic

<220>
 <223> this sequence may also encompass a deletion peptide wherein
 certain positions are absent according to the disclosure

<400> 14
 Gly His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Trp Asp
 20 25 30

<210> 15
 <211> 12
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: EGF-derived
 peptide

<400> 15
 Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys
 1 5 10

<210> 16
 <211> 12
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: EGF-derived
 peptide

<400> 16
 Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
 1 5 10

<210> 17
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: formula
 sequence

<220>
 <221> MOD_RES
 <222> (1)
 <223> unique amino acid, such as cys or lys

<220>
 <221> MOD_RES
 <222> (2)...(3)
 <223> amino acid residue selected to modulate the affinity of
 the internalizing peptide for different membranes

<400> 17
 Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala
 1 5 10 15
 Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
 20 25 30

<210> 18
 <211> 8
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: peptide substrate
 for N-myristoyl transferase

<400> 18
 Gly Asn Ala Ala Ala Arg Arg
 1 5

<210> 19
 <211> 10
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: peptide derived
 from laminin

<400> 19

Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys
 1 5 10

<210> 20

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nde1-EcoR1 fragment

<400> 20

catatgggtg gctgccgtgg cgatatgttc ggttgcggtg ctccctccaaa aaagaagaga 60
 aaggtagctg gattc 75

<210> 21

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: RGD/SV40 peptide

<400> 21

Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys
 1 5 10 15

Lys Lys Arg Lys Val Ala Gly Phe
 20

<210> 22

<211> 225

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nde1-EcoR1 fragment

<400> 22

catatgggagc cagtagatcc tagactagag ccctggaagc atccaggaag tcagcctaaa 60
 actgcttgta ccaattgcta ttgtaaaaag tggtgctttc attgccaagt ttgtttcata 120
 acaaaagccc ttggcatctc ctatggcagg aagaagcgga gacagcgacg aagacctcct 180
 caaggcagtc agactcatca agtttctcta agtaagcaag gattc 225

<210> 23

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: engineered HIV-1 tat

<400> 23

Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
 1 5 10 15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 20 25 30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
 35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
 50 55 60

His Gln Val Ser Leu Ser Lys Gln
 65 70

<210> 24

<211> 912

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nde1-EcoR1 fragment

<400> 24

catatgacct ctgcgcgtc cgtgaagtcg ggtccgcggg aggttccgcg cgatgagtac 60
 gaggatctgt actacacccc gtcttcaggt atggcgagtc ccgatagtcg gcctgacacc 120
 tcccgcggtg gcgcctaca gacacgctcg cgccagaggg gcgaggtccg ttctgtccag 180
 tacgacgagt cggattatgc cctctacggg ggctcgatc ccgaagacga cgaacacccg 240
 gaggtccccc ggacgcggcg tcccgtttcc ggggcggttt tgtccggccc ggggcctgcg 300
 cgggcgcctc cgccacccgc tgggtccgga ggggcgggac gcacaccac caccgcccc 360
 cgggcccccc gaaccacgag ggtggcgact aaggcccccg cgccccggc ggcggagacc 420
 accgcgggca ggaaatcggc ccagccagaa tccgcgcac tcccagacgc cccgcgtcg 480
 acggcgccaa cccgatccaa gacacccgcg caggggctgg ccagaaagct gcactttagc 540
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 aatccagacg tgggtgcagga cgtcgacgcg gccacggcga ctcgagggcg ttctgcggcg 840
 tcgcgccccca ccgagcgacc tcgagcccca gcccgctccg cttctcgcgc cagacggccc 900
 gtcgaggaat tc 912

<210> 25

<211> 301

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: engineered HSV-1 VP22

<400> 25

Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro Arg
 1 5 10 15

Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala Ser
 20 25 30
 Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg
 35 40 45
 Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser Asp
 50 55 60
 Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu
 65 70 75 80
 Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly Pro
 85 90 95
 Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly
 100 105 110
 Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gly Arg Val Ala
 115 120 125
 Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys
 130 135 140
 Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser Thr
 145 150 155 160
 Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu
 165 170 175
 His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro Arg
 180 185 190
 Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu
 195 200 205
 Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met Ser
 210 215 220
 Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr
 225 230 235 240
 Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala Asn
 245 250 255
 Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala
 260 265 270
 Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala
 275 280 285
 Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu
 290 295 300

<210> 26

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nde1-EcoR1 fragment

<400> 26

catatggacg tcgacgcggc cacggcgact cgagggcggt ctgcggcgtc gcgccccacc 60
gagcgacctc gagccccagc ccgctccgct tctcgcccca gacggcccgt cgaggaattc 120

<210> 27

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: VP22 (C-terminal domain)

<400> 27

Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser
1 5 10 15

Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro
20 25 30

Arg Arg Pro Val Glu
35

<210> 28

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic or
natural linker

<400> 28

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 29

<211> 4

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: tetrapeptide
isostere

<400> 29

Ala Ile Tyr Tyr
1

<210> 30
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 30
 gcggatccac catggataam aaagagggac ctaataac 38

<210> 31
 <211> 76
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 31
 ggcggcgccgc ctactcatca tcactagatg gcamcttctg agcaaaacag ccctctggta 60
 ttatagttgt cctcgt 76

<210> 32
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 32
 cgcggcgccgc tactcatcat cactagatgg camttgagcc aaagttttct ctggtattat 60
 agttgtctc gt 72

<210> 33
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> modified_base
 <222> (20)
 <223> i

<220>
 <223> Description of Artificial Sequence: primer

<400> 33
 gcwatccacc atggataatn taaagagggga cctaataac 39

<210> 34

<211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 34
 gtaggtgtat ctccatgtgg tatratagtr gtcc 34

<210> 35
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 35
 ggacaactat aataccacat ggagatacac ctac 34

<210> 36
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 36
 gctcagagtc actcctcctc tgagctgtc 29

<210> 37
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 37
 gcggatccac catggataam aaagaggac ctaataac 38

<210> 38
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 38
 cctatcacat ctatatttta ttggtattat agttgtc 37

<210> 39
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 39
 gacaactata ataccaataa aatatagatg tgatagg 37

<210> 40
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 40
 gcctcgagtc ataatgtggt agtattttgt cctg 34

<210> 41
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 41
 gcggatccac catggaggaa gaagagtata tgcccatgga ggagactctt tgccaacgtt 60
 ttaaattgtg 69

<210> 42
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 42
 gcgcggccgc tcatatagac ataaatccag tagac 35

<210> 43
 <211> 65
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 43

gcggatccgc caccatggac tacaaggacg acgatgacaa agatgacccg gccgaggcgg 60
tgctg 65

<210> 44

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

gtaggtgtat ctccatgtct ggagatgtag gtgtatg 37

<210> 45

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45

catacaccta catctccaga catggagata cacctac 37

<210> 46

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 46

gcgcggccgc tcactcctcc tctgagctgt c 31

<210> 47

<211> 5

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: LFCSE motif

<400> 47

Leu Phe Cys Ser Glu

1

5

<210> 48
 <211> 135
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(135)

<400> 48
 ctg cca gct cgg gga ttg gat cat atc gct gag aac att ctg tca tac 48
 Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr
 1 5 10 15
 ctg gat gcc aaa tca cta tgt gct gct gaa ctt gtg tgc aag gaa tgg 96
 Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys Lys Glu Trp
 20 25 30
 tac cga gtg acc tct gat ggc atg ctg tgg aag aag ctt 135
 Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
 35 40 45

<210> 49
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 49
 Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr
 1 5 10 15
 Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys Lys Glu Trp
 20 25 30
 Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
 35 40 45